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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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EXAMINER	
NEGIN, RUSSELL SCOTT	

ART UNIT	PAPER NUMBER
1631	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	09/923,870	PALSSON, BERNHARD	
	Examiner	Art Unit	
	RUSSELL S. NEGIN	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *15 September 2008*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *49-52,56-60,64 and 68-83* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *49-52,56-60,64 and 68-83* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Comments

Applicants' request for reconsideration in the communication filed on 15 September 2008 is acknowledged.

Claims 49-52, 56-60, 64 and 68-83 are pending and examined in the instant Office action.

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

The following rejection is newly applied:

35 U.S.C. 103 Rejection #1:

Claims 49-52, 56-60, and 68-83 are rejected under 35 U.S.C. 103(a) as being unpatentable over Pramanik et al. [Biotechnology and Bioengineering, volume 56, 1997, pages 398-421] in view of Blattner et al. [Science, volume 277, 1997, pages 1453-1469] in view of Kunst et al. [Reviews in Microbiology, 1991, volume 142, pages 905-912].

Claim 49 is drawn to a method performed in a computer of simulating a metabolic capability of an in silico strain of a microbe, comprising:

--obtaining a plurality of DNA sequences comprising most of the metabolic genes in a genome, to produce an in silico representation of a microbe;

--determining open reading frames of genes of unknown function in the microbe in said plurality of DNA sequences;

--assigning a function to proteins encoded by said open reading frames by determining the homology of said open reading frames to gene sequences encoding proteins of known function;

--determining which of said open reading frames correspond to metabolic genes by determining if the assigned function of said proteins is involved in cellular metabolism;

--determining substrates, products, and stoichiometry of the reaction for each of the gene products of said metabolic genes;

--producing a genome specific stoichiometric matrix of said microbe produced from said substrates, products and stoichiometry;

--determining a metabolic demand corresponding to a biomass composition of said microbe;

--calculating uptake rates of metabolites of said microbe;

--combining said metabolic demands and said uptake rates with said stoichiometric matrix to produce an in silico representation of said microbe;

--incorporating a general linear programming problem to introduce an in silico strain of said microbe;

--performing a flux balance analysis on said in silico strain, and

--providing a visual output to a user of said analysis that simulated a metabolic capability of said strain.

Claim 57 is drawn to a method performed in a computer for simulating a metabolic capability of an in silico strain of a microbe, comprising;

a) providing a nucleotide sequence of a metabolic gene in the microbe;

b) determining substrates, products and stoichiometry of the reaction for the gene product of said metabolic gene, wherein said gene product having an unknown function in the microbe is assigned a function by determining homology of said nucleotide sequence to gene sequences encoding gene products of known function in a different organism;

c) repeating steps a) and b) for most metabolic genes of said microbe to provide an in silico representation;

d) producing a genome specific stoichiometric matrix produced from said substrates, products and stoichiometry of the metabolic gene products in said microbe;

e) determining a metabolic demand corresponding to a biomass composition of said microbe;

f) calculating uptake rates of metabolites of said microbe;

g) combining said metabolic demands and said uptake rates with said stoichiometric matrix to produce an in silico representation of said microbe;

h) incorporating a general linear programming problem to produce an in silico strain of said microbe;

i) performing a flux balance analysis on said in silico strain, and

j) providing a visual output to a user of said analysis that simulated a metabolic capability of said strain.

Claims 50 and 58 are further limiting wherein the microbe is question is E. coli.

Claims 51, 59, 68, 70-72, 75-76, 78-80, and 83 are further limiting wherein cellular metabolism comprises central metabolism, carbohydrate assimilation, lipid and fatty acid metabolism and nucleotide metabolism.

Claims 52 and 60 are further limiting wherein the assigning function comprises performing BLAST.

The study of Pramanik et al. investigates the stoichiometric model of E. coli metabolism, as stated in the abstract:

> A stoichiometric model of metabolism was developed to describe the balance of metabolic reactions during steady state growth of Escherichia coli on glucose (or metabolic intermediates) and mineral salts. The model incorporates 153 reversible and 147 irreversible reactions and 289 metabolites from several metabolic data bases…

Consequently, Pramanik et al. studies many metabolic reactions that take place within E. coli (i.e. see the list in Appendix A on pages 411-417). Equations 1 and 2 on page 399 denote the flux model metabolism via a mass balance on E. coli wherein the matrix S is a matrix of stoichiometric coefficients relevant to the equations.

Table VII on page 405 of Pramanik et al. lists the upper and lower bounds of metabolite uptake and secretion, and the text under this table describes sensitivity of each type of metabolism (i.e. aerobic or anaerobic) due to biomass composition. This biomass and energy requirement (i.e. demand) is elaborated further under “Biomass and energy requirements” in column 2 on page 399 of Pramanik et al.

Again, equations 1 and 2 on page 399 of Pramanik et al. represent a mass balance on the metabolites of E. coli which combines the metabolic demands, uptake rates and the stoichiometric matrix to produce an in silico representation of functions of said microbe.

Page 403 of Pramanik et al., under "Sensitivity Analysis," lists a general linear programming algorithm for solving equations 1 and 2 on page 399 of Pramanik et al.

Figure 3 on page 406 of Pramanik et al. illustrates a flux balance analysis on the in silico strain of E. coli and provides visual output to a user that simulates a metabolic capability of the strain.

However, Pramanik et al. does not teach obtaining a plurality of DNA sequences comprising most of the metabolic genes in an genome, determining open reading frames of these genes, assigning functions to the proteins encoded by the open reading frames, and determining which of said open reading frames correspond to metabolic genes. Additionally, Pramanik et al. does not teach determining open reading frames of genes having an unknown function and assigning a function to their encoded products based on homology to proteins in a different organism.

The study of Blattner et al. maps the complete genome sequence of Escherichia coli K-12.

The final full paragraph of column 3 on page 1454 of Blattner et al. states, "The genome of E. coli, diagrammed in Fig. 1, consists of 4,639,221 bp of complex DNA." Consequently, Figure 1 on page 1465 of Blattner et al. illustrates an *in silico* map of the complete genome of E. coli.

The first full paragraph of column 1 on page 1454 of Blattner et al. describes the annotation process of identifying ORFs in genes constituting operons, regulatory sites, mobile genetic elements, and repetitive sequences in the genome, assigning and suggesting functions, and relating the E coli. sequence to other organisms. The second full paragraph of column 1 on page 1454 states:

> Functions of previously known E. coli proteins were collected from the GenProtEC and EcoCyc database. The function of new translated sequences was inputted from sequence similarity.

Consequently, functions are assigned to proteins by determining similarities (i.e. homologies) to proteins of known function.

The result of assigning functions to proteins is Table 4 on page 1459 of Blattner et al. wherein metabolic genes are classified as such in their specific metabolic classes listed in Table 4 of page 1459 of Blattner et al. One of the classes listed is nucleotide synthesis and metabolism.

The first full paragraph of column 2 on page 1454 of Blattner et al. describes the use of BLAST in assigning function to proteins.

Pramanik et al. and Blattner et al. do not teach determining open reading frames of genes having an unknown function and assigning a function to their encoded products based on homology to proteins in a different organism.

The review of Kunst et al. studies the project of sequencing the entire Bacillus substilis genome. Applicant states in the paragraph bridging columns 1 and 2 on page 905 of Kunst et al.:

> At the first level of analysis, the DNA sequence will lead to a complete catalogue of putative protein sequences. These are likely to fall into one of 3 categories: (1) those whose functions are known, (2) those which show similarities with proteins identified in other organisms and which

> may have similar though not necessarily identical functions in *B. substilis*, and (3) those, probably the majority, whose function is unknown at present....

Consequently, the "unknown" functions of protein sequences are identifiable by homology comparison with corresponding sequences in other organisms. Such analysis allows the identification of function of two proteins with unknown function (see abstract of Kunst et al.).

Kunst et al. continue in the last paragraph of page 905:

> It will be of great interest to compare the sequence of the *B. substilis* genome with that of *E. coli*.... These organisms diverged about 1.2 billion years ago... It will be interesting to examine the conservation of "core" genes responsible for general metabolism.

Consequently, Kunst et al. express great interest in comparing the genomes of *E. coli* and *B. subtilis* as they pertain to metabolism.

Here is a chart illustrating where each of the species in claims 68-83 are found in the above prior art references:

Central metabolism	Claims 68, 76	Kuntz et al., introduction
Amino acid metabolism	Claims 69, 77	TCA cycle in Pramanik et al.
Nucleotide metabolism	Claims 70, 78	TCA cycle in Pramanik et al.
Fatty acid metabolism	Claims 71, 79	Pramanik et al., page 339, c2
Lipid metabolism	Claims 72, 80	Pramanik et al, page 339, c2
Vitamin/co factor synthesis	Claims 73, 81	Appendix A, Pramanik et al.
Energy and redox	Claims 74, 82	Appendix A, Pramanik et al.,
Carbohydrate assimilation	Claims 75, 83	Appendix A, Pramanik et al. and glycolysis

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the stoichiometric model of E. coli metabolism as taught by Pramanik et al. by use of the complete genome sequence of Blattner et al. wherein the motivation would have been that by knowledge of the full genome of E coli, not only can metabolism be further analyzed, but also knowledge of the entire sequence of E. coli enables global approaches to understanding biological function in living cells and has led to new ways of looking at the evolutionary history of bacteria [see first paragraph of introduction on page 1453] It would have been further obvious to modify the stoichiometric model of E. coli metabolism as taught by Pramanik et al. and the complete E. coli genome structure in Blattner et al. by use of the comparison of E. coli and B. substilis metabolism genes and proteins to determine function of unknown proteins as in Kunst et al. wherein the motivation would have been that such homology comparisons allow for an analysis of the differences in evolution between the two different, but related, organisms [see last sentence on page 905 of Kunst et al.].

Response to Arguments:

Applicant's arguments filed 12 August 2008 have been fully considered but they are not persuasive. The newly applied reference of Kunst et al. is used not only to further justify the motivation of combining the studied of Pramanik et al. and Blattner et al., but the reference of Kunst et al. is also used to teach the missing limitation of "determining open reading frames of genes having an unknown function and assigning

a function to their encoded products based on homology to proteins in a different organism."

The following rejection is newly applied:

35 U.S.C. 103 Rejection #2:

Claim 64 is rejected under 35 U.S.C. 103(a) as being unpatentable over Pramanik et al. in view of Blattner et al. in view of Kunst et al. as applied to claims 49-52 and 56-60 above, and further in view of Xie et al. [TIBTECH, 1997, volume 15, pages 109-113].

Pramanik et al., Blattner et al., and Kunst et al. make obvious a method of simulating a metabolic capability of an in silico strain of a microbe by simulating metabolism within E. coli, as discussed above.

Pramanik et al., Blattner et al., and Kunst et al. do not teach calculation of uptake rates by measuring depletion of substrate from the growth media.

The study of Xie et al. studies integrated approaches to the design of media and feeding strategies for fed-batch cultures of animal cells.

Column 2 on page 109, lines 3-7 of Xie et al. states:

> Obviously, a high viable cell density maintained for a long time is required to maximize product concentration. However, this mainly depends upon the composition of the medium employed.

Consequently, the composition of the growth medium and its depletion over time affects the growth of the cells.

The motivation of the study of Xie et al. is that by knowing this fact, better compositions for culture media can be designed (i.e. see page 110 of Xie et al.)

It would have been obvious to someone of ordinary skill in the art at the time of the instant invention to modify the metabolism studies of E. coli of Pramanik et al. Blattner et al., and Kunst et al. by use of the nutrient depletion studies of Xie et al. wherein the motivation would have been by knowing how nutrients are depleted in order to facilitate cell growth, stronger media can be designed to enable better growth of the cells in the cellular media [see page 110, column 1-2 under "Motivation for medium design," and "Design of culture environment."] There would have been a reasonable expectation of success in applying the animal cell study of Xie et al. to the bacterial studies of Pramanik et al. and Blattner et al. because when all cells are cultured, whether animal or bacterial, the cells need nutrients to survive, and as a result, all species of cells deplete their culture media of these nutrients.

Double Patenting

The following rejection is reiterated from the previous Office action:

The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims

are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

Claims 49-52, 56-60 and 64 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 26-28, 30, 32, 35-36, and 39-41 of copending Application No. 11/980,199. Although the conflicting claims are not identical, they are not patentably distinct from each other because the set of claims of the reference describes the same *in silico* process for open reading frames, determining the metabolic capability of a strain of a microbe. For

instance, the steps of claim 30 of '199 correspond with the steps of instant independent claim 49. Each claim has the steps of obtaining DNA sequences, determining ORFs, assigning functions to proteins, determining which open reading frames correspond to metabolic genes, determining a stoichiometric balance on relevant metabolic reactions, determining metabolic demand, calculating uptake rates, combining metabolic demands with uptake rates, incorporating general linear programming, performing a flux balance, and providing visual outputs to a user. Additionally claim 41 of the reference has steps that correspond with the steps of instant independent claim 57.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

Response to Arguments

Applicant's arguments with respect to the instantly rejected claims have been considered but are moot in view of the new ground(s) of rejection (i.e. the double patenting rejection is no longer the sole rejection in the instant Office action).

Conclusion

No claim is allowed.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the central PTO Fax Center. The faxing of such pages must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61

(November 16, 1993), and 1157 OG 94 (December 28, 1993)(See 37 CFR § 1.6(d)). The Central PTO Fax Center Number is (571) 273-8300.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Russell Negin, Ph.D., whose telephone number is (571) 272-1083. The examiner can normally be reached on Monday-Friday from 7am to 4pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's Supervisor, Marjorie Moran, Supervisory Patent Examiner, can be reached at (571) 272-0720.

Information regarding the status of the application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information on the PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

/RSN/
Russell S. Negin
1 December 2008

/Marjorie Moran/
Supervisory Patent Examiner, Art Unit 1631